



Patent Docket P0871P4D2

THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of
Dan L. Eaton et al.
Serial No.: 08/423,194
Filed: 18 April 1995
For: MPL LIGAND

Group Art Unit: 1812

Examiner: L. Spector

CERTIFICATE OF MAILING

I hereby certify that this correspondence is being deposited with the United States Postal Service with sufficient postage as first class mail in an envelope addressed to: Assistant Commissioner of Patents, Washington, D.C. 20231 on

January 2, 1997

Joyce Cohen
Joyce Cohen

CERTIFICATE RE: SEQUENCE LISTING

RESPONSE UNDER 37 CFR § 1.821(f) and (g)

Assistant Commissioner of Patents
Washington, D.C. 20231

Sir:

I hereby state that the Sequence Listing submitted herewith is submitted in paper copy and a computer-readable diskette, and that the content of the paper and computer readable copies are the same. I further state that this submission includes no new matter.

Respectfully submitted,

GENENTECH, INC.

By: *Daryl B. Winter*
Daryl B. Winter
Reg. No. 32,637

Date: January 2, 1997

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NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 CFR 1.821 - 1.825 for the following reason(s):

1. This application clearly fails to comply with the requirements of 37 CFR 1.821 - 1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.

2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 CFR 1.821(c).

3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 CFR 1.821(e).

4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 CFR 1.822 and/or 1.823, as indicated on the attached copy of the marked-up "Raw Sequence Listing."

5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A substitute computer readable form must be submitted as required by 37 CFR 1.825(d).

6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 CFR 1.821(e).

7. Seq 1125 is Reversed polarity
Other: _____

Applicant must provide:

An initial or substitute computer readable form (CRF) copy of the "Sequence Listing"

An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification

A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 CFR 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d)

For questions regarding compliance with these requirements, please contact:

For Rules Interpretation, call (703) 308-1123

For CRF submission help, call (703) 308-4212

For PatentIn software help, call (703) 557-0400

Please return a copy of this notice with your response.



SEQUENCE LISTING

(1) GENERAL INFORMATION:

5 (i) APPLICANT: Eaton, Dan L.
de Sauvage, Frederic J.

(ii) TITLE OF INVENTION: MPL LIGAND

10 (iii) NUMBER OF SEQUENCES: 77

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Genentech, Inc.
(B) STREET: 460 Point San Bruno Blvd
15 (C) CITY: South San Francisco
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 94080

20 (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: patin (Genentech)

25 (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/423194
(B) FILING DATE: 18-APR-1995
(C) CLASSIFICATION:

30 (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/249376
(B) FILING DATE: 25-MAY-1994

35 (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/223263
(B) FILING DATE: 04-APR-1994

40 (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/196689
(B) FILING DATE: 15-FEB-1994

45 (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/185607
(B) FILING DATE: 21-JAN-1994

50 (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/176553
(B) FILING DATE: 03-JAN-1994

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Winter, Daryl B.

(B) REGISTRATION NUMBER: 32,637
(C) REFERENCE/DOCKET NUMBER: 871P4D2

5 (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 415/225-1249
(B) TELEFAX: 415/952-9881
(C) TELEX: 910/371-7168

10 (2) INFORMATION FOR SEQ ID NO:1:

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 353 amino acids
(B) TYPE: amino acid
(C) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Glu Leu Thr Glu Leu Leu Leu Val Val Met Leu Leu Leu Thr
-21 -20 -15 -10

20 Ala Arg Leu Thr Leu Ser Ser Pro Ala Pro Pro Ala Cys Asp Leu
-5 1 5

25 Arg Val Leu Ser Lys Leu Leu Arg Asp Ser His Val Leu His Ser
10 15 20

Arg Leu Ser Gln Cys Pro Glu Val His Pro Leu Pro Thr Pro Val
25 30 35

30 Leu Leu Pro Ala Val Asp Phe Ser Leu Gly Glu Trp Lys Thr Gln
40 45 50

B
Cont³⁵
Met Glu Glu Thr Lys Ala Gln Asp Ile Leu Gly Ala Val Thr Leu
55 60 65

Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln Leu Gly Pro Thr
70 75 80

40 Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser Gly Gln Val Arg Leu
85 90 95

Leu Leu Gly Ala Leu Gln Ser Leu Leu Gly Thr Gln Leu Pro Pro
100 105 110

45 Gln Gly Arg Thr Thr Ala His Lys Asp Pro Asn Ala Ile Phe Leu
115 120 125

Ser Phe Gln His Leu Leu Arg Gly Lys Val Arg Phe Leu Met Leu
130 135 140

50 Val Gly Gly Ser Thr Leu Cys Val Arg Arg Ala Pro Pro Thr Thr
145 150 155

Ala Val Pro Ser Arg Thr Ser Leu Val Leu Thr Leu Asn Glu Leu
160 165 170

5 Pro Asn Arg Thr Ser Gly Leu Leu Glu Thr Asn Phe Thr Ala Ser
175 180 185

Ala Arg Thr Thr Gly Ser Gly Leu Leu Lys Trp Gln Gln Gly Phe
190 195 200

10 Arg Ala Lys Ile Pro Gly Leu Leu Asn Gln Thr Ser Arg Ser Leu
205 210 215

Asp Gln Ile Pro Gly Tyr Leu Asn Arg Ile His Glu Leu Leu Asn
220 225 230

15 Gly Thr Arg Gly Leu Phe Pro Gly Pro Ser Arg Arg Thr Leu Gly
235 240 245

Ala Pro Asp Ile Ser Ser Gly Thr Ser Asp Thr Gly Ser Leu Pro
20 250 255 260

Pro Asn Leu Gln Pro Gly Tyr Ser Pro Ser Pro Thr His Pro Pro
265 270 275

25 Thr Gly Gln Tyr Thr Leu Phe Pro Leu Pro Pro Thr Leu Pro Thr
280 285 290

Pro Val Val Gln Leu His Pro Leu Leu Pro Asp Pro Ser Ala Pro
295 300 305

30 *1/* Thr Pro Thr Pro Thr Ser Pro Leu Leu Asn Thr Ser Tyr Thr His
310 315 320

cont
35 Ser Gln Asn Leu Ser Gln Glu Gly
325 330 332

(2) INFORMATION FOR SEQ ID NO:2:

40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1795 bases
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TCTTCCTTACCATCTGCTCC CCAGAGGGCT GCCTGCTGTG CACTTGGGTC 50

50 CTGGAGCCCT TCTCCACCCG GATAGATTCC TCACCCCTTGG CCCGCCTTTG 100

CCCCACCCCTA CTCTGCCAG AAGTGCAAGA GCCTAAGCCG CCTCCATGGC 150
5 CCCAGGAAGG ATTCAGGGGA GAGGCCCAA ACAGGGAGCC ACGCCAGCCA 200
GACACCCCGG CCAGAATGGA GCTGACTGAA TTGCTCCTCG TGGTCATGCT 250
10 TCTCCTAACT GCAAGGCTAA CGCTGTCCAG CCCGGCTCCT CCTGCTTGTG 300
ACCTCCGAGT CCTCAGTAAA CTGCTTCGTG ACTCCCATGT CCTTCACAGC 350
15 AGACTGAGCC AGTGCCAGA GGTCACCCCT TTGCCTACAC CTGTCCTGCT 400
20 GCCTGCTGTG GACTTTAGCT TGGGAGAATG GAAAACCCAG ATGGAGGAGA 450
CCAAGGCACA GGACATTCTG GGAGCAGTGA CCCTTCTGCT GGAGGGAGTG 500
25 ATGGCAGCAC GGGGACAACACT GGGACCCACT TGCCTCTCAT CCCTCCTGGG 550
GCAGCTTCT GGACAGGTCC GTCTCCTCCT TGGGGCCCTG CAGAGCCTCC 600
30 TTGGAACCCA GCTTCCTCCA CAGGGCAGGA CCACAGCTCA CAAGGATCCC 650
AATGCCATCT TCCTGAGCTT CCAACACCTG CTCCGAGGAA AGGTGCGTTT 700
35 CCTGATGCTT GTAGGAGGGT CCACCCCTCTG CGTCAGGCAG GCCCCACCCA 750
40 CCACAGCTGT CCCCAGCAGA ACCTCTCTAG TCCTCACACT GAACGAGCTC 800
CCAAACAGGA CTTCTGGATT GTTGGAGACA AACTTCACTG CCTCAGCCAG 850
45 AACTACTGGC TCTGGGCTTC TGAAGTGGCA GCAGGGATTC AGAGCCAAGA 900
TTCCTGGTCT GCTGAACCAA ACCTCCAGGT CCCTGGACCA AATCCCCGGA 950
50 TACCTGAACA GGATACACGA ACTCTTGAAT GGAACTCGTG GACTCTTCC 1000

TGGACCCTCA CGCAGGACCC TAGGAGCCCC GGACATTCC TCAGGAACAT 1050

5 CAGACACAGG CTCCCTGCCA CCCAACCTCC AGCCTGGATA TTCTCCTTCC 1100

CCAACCCATC CTCCTACTGG ACAGTATAcg CTCTTCCCTC TTCCACCCAC 1150

10 CTTGCCACC CCTGTGGTCC AGCTCCACCC CCTGCTTCCT GACCCTTCTG 1200

15 CTCCAACGCC CACCCCTACC AGCCCTCTTC TAAACACATC CTACACCCAC 1250

TCCCAGAACATC TGTCTCAGGA AGGGTAAGGT TCTCAGACAC TGCCGACATC 1300

20 AGCATTGTCT CATGTACAGC TCCCTCCCT GCAGGGCGCC CCTGGGAGAC 1350

AACTGGACAA GATTCCTAC TTTCTCCTGA AACCCAAAGC CCTGGTAAAA 1400

25 GGGATACACA GGACTGAAAA GGGAAATCATT TTTCACTGTA CATTATAAAC 1450

30 CTTCAGAAC TATTTTTTA AGCTATCAGC AATACTCATC AGAGCAGCTA 1500

35 GCTCTTGGT CTATTTCTG CAGAAATTG CAACTCACTG ATTCTCTACA 1550

TGCTTTTTT CTGTGATAAC TCTGCAAAGG CCTGGGCTGG CCTGGCAGTT 1600

GAACAGAGGG AGAGACTAAC CTTGAGTCAG AAAACAGAGA AAGGGTAATT 1650

40 TCCTTGCTT CAAATTCAAG GCCTTCAAAC GCCCCCATCC CCTTTACTAT 1700

45 CATTCTCAGT GGGACTCTGA TCCCATATTG TTAACAGATC TTTACTCTG 1750

AGAAATGAAT AAGCTTCTC TCAGAAAAAA AAAAAAAA AAAAA 1795

50

(2) INFORMATION FOR SEQ ID NO:3:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Leu Leu Leu Val Val Met Leu Leu Leu Thr Ala Arg Leu Thr Leu
-16 -15 -10 -5

10 Ser Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys
1 5 10

15 Leu Leu Arg Asp Ser His Val Leu His Ser Arg Leu
15 20 25 26

20 (2) INFORMATION FOR SEQ ID NO:4:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 390 bases
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GAATTCCCTGG AATACCAGCT GACAATGATT TCCTCCTCAT CTTTCAACCT 50

30 CACCTCTCCT CATCTAAGAA TTGCTCCTCG TGGTCATGCT TCTCCTAACT 100

35 GCAAGGCTAA CGCTGTCCAG CCCGGCTCCT CCTGCTTG TG ACCTCCGAGT 150

CCTCAGTAAA CTGCTTCGTG ACTCCCATGT CCTTCACAGC AGACTGGTGA 200

40 GAACTCCCAA CATTATCCCC TTTATCCGCG TAACTGGTAA GACACCCATA 250

CTCCCAGGAA GACACCATCA CTTCCTCTAA CTCCTTGACC CAATGACTAT 300

45 TCTTCCCATA TTGTCCCCAC CTACTGATCA CACTCTCTGA CAAGAATTAT 350

50 TCTTCACAAT ACAGCCCGCA TTTAAAAGCT CTCGTCTAGA 390

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

10 TCTAGACGAG AGCTTTAAA TGCAGGCTGT ATTGTGAAGA ATAATTCTTG 50
TCAGAGAGTG TGATCAGTAG GTGGGGACAA TATGGGAAGA ATAGTCATTG 100
15 GGTCAAGGAG TTAGAGGAAG TGATGGTGTGTC TTCCTGGGAG TATGGGTGTC 150
TTACCAAGTTA CGCGGATAAAA GGGGATAATG TTGGGAGTTC TCACCAAGTCT 200
20 GCTGTGAAGG ACATGGGAGT CACGAAGCAG TTTACTGAGG ACTCGGAGGT 250
CACAAAGCAGG AGGAGCCGGG CTGGACAGCG TTAGCCTTGC AGTTAGGAGA 300
AGCATGACCA CGAGGAGCAA TTCTTAGATG AGGAGAGGTG AGGTTGAAAG 350
25 ATGAGGAGGA AATCATTGTC AGCTGGTATT CCAGGAATTC 390

(2) INFORMATION FOR SEQ ID NO:6:

30 |
1 (i) SEQUENCE CHARACTERISTICS:
35 (A) LENGTH: 332 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

35 Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys Leu
1 5 10 15
40 Leu Arg Asp Ser His Val Leu His Ser Arg Leu Ser Gln Cys Pro
20 25 30
45 Glu Val His Pro Leu Pro Thr Pro Val Leu Leu Pro Ala Val Asp
35 40 45
50 Phe Ser Leu Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys Ala
50 55 60
Gln Asp Ile Leu Gly Ala Val Thr Leu Leu Glu Gly Val Met
65 70 75

Ala Ala Arg Gly Gln Leu Gly Pro Thr Cys Leu Ser Ser Leu Leu
 80 85 90

5 Gly Gln Leu Ser Gly Gln Val Arg Leu Leu Leu Gly Ala Leu Gln
 95 100 105

Ser Leu Leu Gly Thr Gln Leu Pro Pro Gln Gly Arg Thr Thr Ala
 110 115 120

10 His Lys Asp Pro Asn Ala Ile Phe Leu Ser Phe Gln His Leu Leu
 125 130 135

Arg Gly Lys Val Arg Phe Leu Met Leu Val Gly Gly Ser Thr Leu
 140 145 150

15 Cys Val Arg Arg Ala Pro Pro Thr Thr Ala Val Pro Ser Arg Thr
 155 160 165

20 Ser Leu Val Leu Thr Leu Asn Glu Leu Pro Asn Arg Thr Ser Gly
 170 175 180

Leu Leu Glu Thr Asn Phe Thr Ala Ser Ala Arg Thr Thr Gly Ser
 185 190 195

25 Gly Leu Leu Lys Trp Gln Gln Gly Phe Arg Ala Lys Ile Pro Gly
 200 205 210

Leu Leu Asn Gln Thr Ser Arg Ser Leu Asp Gln Ile Pro Gly Tyr
 215 220 225

30 Leu Asn Arg Ile His Glu Leu Leu Asn Gly Thr Arg Gly Leu Phe
 230 235 240

B |
 35 Pro Gly Pro Ser Arg Arg Thr Leu Gly Ala Pro Asp Ile Ser Ser
 245 250 255

Gly Thr Ser Asp Thr Gly Ser Leu Pro Pro Asn Leu Gln Pro Gly
 260 265 270

40 Tyr Ser Pro Ser Pro Thr His Pro Pro Thr Gly Gln Tyr Thr Leu
 275 280 285

Phe Pro Leu Pro Pro Thr Leu Pro Thr Pro Val Val Gln Leu His
 290 295 300

Pro Leu Leu Pro Asp Pro Ser Ala Pro Thr Pro Thr Pro Thr Ser
 305 310 315

50 Pro Leu Leu Asn Thr Ser Tyr Thr His Ser Gln Asn Leu Ser Gln
 320 325 330

Glu Gly
332

5 (2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 166 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

15 Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr
1 5 10 15

Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala
20 25 30

20 Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys
35 40 45

Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala
50 55 60

25 Val Glu Val Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu
65 70 75

30 Arg Gly Gln Ala Leu Leu Val Asn Ser Ser Gln Pro Trp Glu Pro
80 85 90

Leu Gln Leu His Val Asp Lys Ala Val Ser Gly Leu Arg Ser Leu
95 100 105

35 Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu Ala Ile Ser
110 115 120

Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala
125 130 135

40 Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg
140 145 150

45 Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp
155 160 165

Arg
166

50 (2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

	Ser	Pro	Ala	Pro	Pro	Ala	Cys	Asp	Leu	Arg	Val	Leu	Ser	Lys	Leu
	1					5				10					15
10	Leu	Arg	Asp	Ser	His	Val	Leu	His	Ser	Arg	Leu	Ser	Gln	Cys	Pro
						20				25					30
15	Glu	Val	His	Pro	Leu	Pro	Thr	Pro	Val	Leu	Leu	Pro	Ala	Val	Asp
						35				40					45
	Phe	Ser	Leu	Gly	Glu	Trp	Lys	Thr	Gln	Met	Glu	Glu	Thr	Lys	Ala
						50				55					60
20	Gln	Asp	Ile	Leu	Gly	Ala	Val	Thr	Leu	Leu	Glu	Gly	Val	Met	
						65			70						75
	Ala	Ala	Arg	Gly	Gln	Leu	Gly	Pro	Thr	Cys	Leu	Ser	Ser	Leu	Leu
						80				85					90
25	Gly	Gln	Leu	Ser	Gly	Gln	Val	Arg	Leu	Leu	Leu	Gly	Ala	Leu	Gln
						95				100					105
30	Ser	Leu	Leu	Gly	Thr	Gln	Gly	Arg	Thr	Thr	Ala	His	Lys	Asp	Pro
						110			115						120
	Asn	Ala	Ile	Phe	Leu	Ser	Phe	Gln	His	Leu	Leu	Arg	Gly	Lys	Val
						125				130					135
35	Arg	Phe	Leu	Met	Leu	Val	Gly	Gly	Ser	Thr	Leu	Cys	Val	Arg	Arg
						140			145						150
	Ala	Pro	Pro	Thr	Thr	Ala	Val	Pro	Ser	Arg	Thr	Ser	Leu	Val	Leu
						155			160						165
40	Thr	Leu	Asn	Glu	Leu	Pro	Asn	Arg	Thr	Ser	Gly	Leu	Leu	Glu	Thr
						170			175						180
45	Asn	Phe	Thr	Ala	Ser	Ala	Arg	Thr	Thr	Gly	Ser	Gly	Leu	Leu	Lys
						185				190					195
	Trp	Gln	Gln	Gly	Phe	Arg	Ala	Lys	Ile	Pro	Gly	Leu	Leu	Asn	Gln
						200				205					210
50	Thr	Ser	Arg	Ser	Leu	Asp	Gln	Ile	Pro	Gly	Tyr	Leu	Asn	Arg	Ile
						215			220						225

His	Glu	Leu	Leu	Asn	Gly	Thr	Arg	Gly	Leu	Phe	Pro	Gly	Pro	Ser	
														240	
														230	
														235	
5	Arg	Arg	Thr	Leu	Gly	Ala	Pro	Asp	Ile	Ser	Ser	Gly	Thr	Ser	Asp
														255	
														245	
														250	
	Thr	Gly	Ser	Leu	Pro	Pro	Asn	Leu	Gln	Pro	Gly	Tyr	Ser	Pro	Ser
														270	
10	Pro	Thr	His	Pro	Pro	Thr	Gly	Gln	Tyr	Thr	Leu	Phe	Pro	Leu	Pro
														285	
														275	
														280	
15	Pro	Thr	Leu	Pro	Thr	Pro	Val	Val	Gln	Leu	His	Pro	Leu	Leu	Pro
														300	
														290	
														295	
	Asp	Pro	Ser	Ala	Pro	Thr	Pro	Thr	Pro	Thr	Ser	Pro	Leu	Leu	Asn
														315	
														305	
20	Thr	Ser	Tyr	Thr	His	Ser	Gln	Asn	Leu	Ser	Gln	Glu	Gly		
														328	
														320	
														325	

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Ser	Pro	Ala	Pro	Pro	Ala	Cys	Asp	Leu	Arg	Val	Leu	Ser	Lys	Leu	
1					5					10				15	
35	Leu	Arg	Asp	Ser	His	Val	Leu	His	Ser	Arg	Leu	Ser	Gln	Cys	Pro
						20				25					30
40	Glu	Val	His	Pro	Leu	Pro	Thr	Pro	Val	Leu	Leu	Pro	Ala	Val	Asp
						35				40					45
45	Phe	Ser	Leu	Gly	Glu	Trp	Lys	Thr	Gln	Met	Glu	Glu	Thr	Lys	Ala
						50				55					60
50	Gln	Asp	Ile	Leu	Gly	Ala	Val	Thr	Leu	Leu	Leu	Glu	Gly	Val	Met
						65				70					75
55	Ala	Ala	Arg	Gly	Gln	Leu	Gly	Pro	Thr	Cys	Leu	Ser	Ser	Leu	Leu
						80				85					90
60	Gly	Gln	Leu	Ser	Gly	Gln	Val	Arg	Leu	Leu	Leu	Gly	Ala	Leu	Gln
															105

Ser Leu Leu Gly Thr Gln Leu Pro Pro Gln Gly Arg Thr Thr Ala
 110 115 120
 His Lys Asp Pro Asn Ala Ile Phe Leu Ser Phe Gln His Leu Leu
 5 125 130 135
 Arg Gly Lys Asp Phe Trp Ile Val Gly Asp Lys Leu His Cys Leu
 140 145 150
 10 Ser Gln Asn Tyr Trp Leu Trp Ala Ser Glu Val Ala Ala Gly Ile
 155 160 165
 Gln Ser Gln Asp Ser Trp Ser Ala Glu Pro Asn Leu Gln Val Pro
 15 170 175 180
 Gly Pro Asn Pro Arg Ile Pro Glu Gln Asp Thr Arg Thr Leu Glu
 185 190 195
 20 Trp Asn Ser Trp Thr Leu Ser Trp Thr Leu Thr Gln Asp Pro Arg
 200 205 210
 Ser Pro Gly His Phe Leu Arg Asn Ile Arg His Arg Leu Pro Ala
 215 220 225
 25 Thr Gln Pro Pro Ala Trp Ile Phe Ser Phe Pro Asn Pro Ser Ser
 230 235 240
 Tyr Trp Thr Val Tyr Ala Leu Pro Ser Ser Thr His Leu Ala His
 30 245 250 255
 Pro Cys Gly Pro Ala Pro Pro Pro Ala Ser
 260 265

B
35 (2) INFORMATION FOR SEQ ID NO:10:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 261 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys Leu
 45 1 5 10 15
 Leu Arg Asp Ser His Val Leu His Ser Arg Leu Ser Gln Cys Pro
 20 25 30
 50 Glu Val His Pro Leu Pro Thr Pro Val Leu Leu Pro Ala Val Asp
 35 40 45

Phe Ser Leu Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys Ala
 50 55 60

5 Gln Asp Ile Leu Gly Ala Val Thr Leu Leu Leu Glu Gly Val Met
 65 70 75

Ala Ala Arg Gly Gln Leu Gly Pro Thr Cys Leu Ser Ser Leu Leu
 80 85 90

10 Gly Gln Leu Ser Gly Gln Val Arg Leu Leu Leu Gly Ala Leu Gln
 95 100 105

Ser Leu Leu Gly Thr Gln Gly Arg Thr Thr Ala His Lys Asp Pro
 110 115 120

15 Asn Ala Ile Phe Leu Ser Phe Gln His Leu Leu Arg Gly Lys Asp
 125 130 135

20 Phe Trp Ile Val Gly Asp Lys Leu His Cys Leu Ser Gln Asn Tyr
 140 145 150

Trp Leu Trp Ala Ser Glu Val Ala Ala Gly Ile Gln Ser Gln Asp
 155 160 165

25 Ser Trp Ser Ala Glu Pro Asn Leu Gln Val Pro Gly Pro Asn Pro
 170 175 180

Arg Ile Pro Glu Gln Asp Thr Arg Thr Leu Glu Trp Asn Ser Trp
 185 190 195

30 Thr Leu Ser Trp Thr Leu Thr Gln Asp Pro Arg Ser Pro Gly His
 200 205 210

35 Phe Leu Arg Asn Ile Arg His Arg Leu Pro Ala Thr Gln Pro Pro
 215 220 225

Ala Trp Ile Phe Ser Phe Pro Asn Pro Ser Ser Tyr Trp Thr Val
 230 235 240

40 Tyr Ala Leu Pro Ser Ser Thr His Leu Ala His Pro Cys Gly Pro
 245 250 255

45 Ala Pro Pro Pro Ala Ser
 260 261

(2) INFORMATION FOR SEQ ID NO:11:

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1443 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

5 GAGTCCTTGG CCCACCTCTC TCCCACCCGA CTCTGCCGAA AGAAGCACAG 50
10 AAGCTCAAGC CGCCTCCATG GCCCCAGGAA AGATTCAAGGG GAGAGGCC 100
15 ATACAGGGAG CCACTTCAGT TAGACACCCT GGCCAGAATG GAGCTGACTG 150
20 ATTTGCTCCT GGCAGGCCATG CTTCTTGCAG TGGCAAGACT AACTCTGTCC 200
25 AGCCCCGTAG CTCCTGCCTG TGACCCCAGA CTCCTAAATA AACTGCTGCG 250
30 TGACTCCCAC CTCCTTCACA GCCGACTGAG TCAGTGTCCC GACGTCGACC 300
35 CTTTGTCTAT CCCTGTTCTG CTGCCTGCTG TGGACTTTAG CCTGGGAGAA 350
40 TGGAAAACCC AGACGGAACA GAGCAAGGCA CAGGACATTG TAGGGGCAGT 400
45 GTCCCTTCTA CTGGAGGGAG TGATGGCAGC ACGAGGACAG TTGGAACCC 450
50 *cont* CCTGCCTCTC ATCCCTCCTG GGACAGCTTT CTGGGCAGGT TCGCCTCCTC 500
55 TTGGGGGCCCT TGCAGGGCCT CCTAGGAACC CAGGGCAGGA CCACAGCTCA 550
60 CAAGGACCCC AATGCCCTCT TCTTGAGCTT GCAACAACTG CTTGGGGAA 600
65 AGGTGCGCTT CCTGTTCTG GTAGAAGGTC CCACCCCTTG TGTCAGACGG 650
70 ACCCTGCCAA CCACAGCTGT CCCAAGCAGT ACTTCTCAAC TCCTCACACT 700
75 AAACAAGTTC CCAAACAGGA CTTCTGGATT GTTGGAGACG AACTTCAGTG 750
80 50 TCACAGGCCAG AACTGCTGGC CCTGGACTTC TGAGCAGGCT TCAGGGATTC 800

AGAGTCAAGA TTACTCCTGG TCAGCTAAAT CAAACCTCCA GGTCCCCAGT 850

5 CCAAATCTCT GGATACCTGA ACAGGACACA CGGACCTGTG AATGGAACTC 900

ATGGGCTCTT TGCTGGAACC TCACTTCAGA CCCTGGAAGC CTCAGACATC 950

10 TCGCCCGGAG CTTTCAACAA AGGCTCCCTG GCATTCAACC TCCAGGGTGG 1000

ACTTCCTCCT TCTCCAAGCC TTGCTCCTGA TGGACACACA CCCTCCCTC 1050

15 CTTCACCTGC CTTGCCACC ACCCATGGAT CTCCACCCCC GCTCCACCCCC 1100

20 CTGTTTCCTG ACCCTTCCAC CACCATGCCT AACTCTACCG CCCCTCATCC 1150

AGTCACAATG TACCCCTCATC CCAGGAATT GTCTCAGGAA ACATAGCGCG 1200

25 GGCACTGGCC CAGTGAGCGT CTGCAGCTTC TCTCGGGGAC AAGCTTCCCC 1250

AGGAAGGCTG AGAGGCAGCT GCATCTGCTC CAGATGTTCT GCTTCACCT 1300

30 AAAAGGCCCT GGGGAAGGGA TACACAGCAC TGGAGATTGT AAAATTTAG 1350

35 GAGCTATTTT TTTTAACCT ATCAGCAATA TTCATCAGAG CAGCTAGCGA 1400

TCTTTGGTCT ATTTTCGGTA TAAATTGAA AATCACTAAT TCT 1443

40

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 352 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

50 Met Glu Leu Thr Asp Leu Leu Leu Ala Ala Met Leu Leu Ala Val
-21 -20 -15 -10

Ala Arg Leu Thr Leu Ser Ser Pro Val Ala Pro Ala Cys Asp Pro
-5 1 5

5 Arg Leu Leu Asn Lys Leu Leu Arg Asp Ser His Leu Leu His Ser
10 15 20

Arg Leu Ser Gin Cys Pro Asp Val Asp Pro Leu Ser Ile Pro Val
25 30 35

10 Leu Leu Pro Ala Val Asp Phe Ser Leu Gly Glu Trp Lys Thr Gln
40 45 50

Thr Glu Gln Ser Lys Ala Gln Asp Ile Leu Gly Ala Val Ser Leu
55 60 65

15 Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln Leu Glu Pro Ser
70 75 80

20 Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser Gly Gln Val Arg Leu
85 90 95

Leu Leu Gly Ala Leu Gln Gly Leu Leu Gly Thr Gln Gly Arg Thr
100 105 110

25 Thr Ala His Lys Asp Pro Asn Ala Leu Phe Leu Ser Leu Gln Gln
115 120 125

Leu Leu Arg Gly Lys Val Arg Phe Leu Leu Leu Val Glu Gly Pro
130 135 140

30 Thr Leu Cys Val Arg Arg Thr Leu Pro Thr Thr Ala Val Pro Ser
145 150 155

35 Ser Thr Ser Gln Leu Leu Thr Leu Asn Lys Phe Pro Asn Arg Thr
160 165 170

Ser Gly Leu Leu Glu Thr Asn Phe Ser Val Thr Ala Arg Thr Ala
175 180 185

40 Gly Pro Gly Leu Leu Ser Arg Leu Gln Gly Phe Arg Val Lys Ile
190 195 200

45 Thr Pro Gly Gln Leu Asn Gln Thr Ser Arg Ser Pro Val Gln Ile
205 210 215

Ser Gly Tyr Leu Asn Arg Thr His Gly Pro Val Asn Gly Thr His
220 225 230

50 Gly Leu Phe Ala Gly Thr Ser Leu Gln Thr Leu Glu Ala Ser Asp
235 240 245

Ile Ser Pro Gly Ala Phe Asn Lys Gly Ser Leu Ala Phe Asn Leu
250 255 260

5 Gln Gly Gly Leu Pro Pro Ser Pro Ser Leu Ala Pro Asp Gly His
265 270 275

Thr Pro Phe Pro Pro Ser Pro Ala Leu Pro Thr Thr His Gly Ser
280 285 290

10 Pro Pro Gln Leu His Pro Leu Phe Pro Asp Pro Ser Thr Thr Met
295 300 305

Pro Asn Ser Thr Ala Pro His Pro Val Thr Met Tyr Pro His Pro
310 315 320

15 Arg Asn Leu Ser Gln Glu Thr
325 330 331

(2) INFORMATION FOR SEQ ID NO:13:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1536 bases
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

30 GAGTCCTTGG CCCACCTCTC TCCCACCCGA CTCTGCCGAA AGAACACAG 50
1
cont
35 AAGCTCAAGC CGCCTCCATG GCCCCAGGAA AGATTCAGGG GAGAGGCC 100
ATACAGGGAG CCACTTCAGT TAGACACCCT GGCCAGAATG GAGCTGACTG 150
40 ATTTGCTCCT GGCGGCCATG CTTCTTGCAG TGGCAAGACT AACTCTGTCC 200
AGCCCCGTAG CTCCTGCCTG TGACCCCAGA CTCCTAAATA AACTGCTGCG 250
45 TGACTCCCAC CTCCTTCACA GCCGACTGAG TCAGTGTCCC GACGTCGACC 300
CTTTGTCTAT CCCTGTTCTG CTGCCTGCTG TGGACTTTAG CCTGGGAGAA 350
50 TGGAAAACCC AGACGGAACA GAGCAAGGCA CAGGACATTG TAGGGGCAGT 400

GTCCCTTCTA CTGGAGGGAG TGATGGCAGC ACGAGGACAG TTGGAACCCT 450
5 CCTGCCTCTC ATCCCTCCTG GGACAGCTT CTGGGCAGGT TCGCCTCCTC 500
TTGGGGGCCCTG CCGAGGACCC CAGCTTCCTC TACAGGGCAG 550
10 GACCACAGCT CACAAGGACC CCAATGCCCT CTTCTTGAGC TTGCAACAAAC 600
TGCTTCGGGG AAAGGTGCGC TTCCCTGCTTC TGGTAGAAGG TCCCACCCCTC 650
15 TGTGTCAGAC GGACCCTGCC AACCACAGCT GTCCCAAGCA GTACTTCTCA 700
ACTCCTCACA CTAAACAAGT TCCCAAACAG GACTTCTGGA TTGTTGGAGA 750
20 CGAACTTCAG TGTCACAGCC AGAACTGCTG GCCCTGGACT TCTGAGCAGG 800
25 CTTCAGGGAT TCAGAGTCAA GATTACTCCT GGTCAGCTAA ATCAAACCTC 850
CAGGTCCCCA GTCCAAATCT CTGGATACCT GAACAGGACA CACGGACCTG 900
30 TGAATGGAAC TCATGGGCTC TTTGCTGGAA CCTCACTTCA GACCCTGGAA 950
1 GCCTCAGACA TCTCGCCCGG AGCTTCAAC AAAGGCTCCC TGGCATTCAA 1000
35 CCTCCAGGGT GGACTTCCTC CTTCTCCAAG CCTTGCTCCT GATGGACACA 1050
40 CACCCCTTCCC TCCTTCACCT GCCTTGCCCA CCACCCATGG ATCTCCACCC 1100
CAGCTCCACC CCCTGTTCC TGACCCCTCC ACCACCATGC CTAACCTAC 1150
45 CGCCCCTCAT CCAGTCACAA TGTACCCCTCA TCCCAGGAAT TTGTCTCAGG 1200
AAACATAGCG CGGGCACTGG CCCAGTGAGC GTCTGCAGCT TCTCTCGGGG 1250
50 ACAAGCTTCC CCAGGAAGGC TGAGAGGCAG CTGCATCTGC TCCAGATGTT 1300

CTGCTTCAC CTAAGGCC CTGGGAAGG GATACACAGC ACTGGAGATT 1350

5 GTAAAATTT AGGAGCTATT TTTTTAAC CTATCAGCAA TATTCATCAG 1400

AGCAGCTAGC GATCTTGTT CTATTTCGG TATAAATTG AAAATCACTA 1450

10 AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA 1500

15 AAAAAAAA AAAAAAAA AAAAAAAA AAAAAA 1536

(2) INFORMATION FOR SEQ ID NO:14:

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 356 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Glu Leu Thr Asp Leu Leu Leu Ala Ala Met Leu Leu Ala Val
-21 -20 -15 -10

30 Ala Arg Leu Thr Leu Ser Ser Pro Val Ala Pro Ala Cys Asp Pro
-5 1 5

Arg Leu Leu Asn Lys Leu Leu Arg Asp Ser His Leu Leu His Ser
10 15 20

35 Arg Leu Ser Gln Cys Pro Asp Val Asp Pro Leu Ser Ile Pro Val
25 30 35

Leu Leu Pro Ala Val Asp Phe Ser Leu Gly Glu Trp Lys Thr Gln
40 45 50

Thr Glu Gln Ser Lys Ala Gln Asp Ile Leu Gly Ala Val Ser Leu
55 60 65

45 Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln Leu Glu Pro Ser
70 75 80

Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser Gly Gln Val Arg Leu
85 90 95

50 Leu Leu Gly Ala Leu Gln Gly Leu Leu Gly Thr Gln Leu Pro Leu
100 105 110

Gln Gly Arg Thr Thr Ala His Lys Asp Pro Asn Ala Leu Phe Leu
 115 120 125

5 Ser Leu Gln Gln Leu Leu Arg Gly Lys Val Arg Phe Leu Leu Leu
 130 135 140

Val Glu Gly Pro Thr Leu Cys Val Arg Arg Thr Leu Pro Thr Thr
 145 150 155

10 Ala Val Pro Ser Ser Thr Ser Gln Leu Leu Thr Leu Asn Lys Phe
 160 165 170

Pro Asn Arg Thr Ser Gly Leu Leu Glu Thr Asn Phe Ser Val Thr
 175 180 185

15 Ala Arg Thr Ala Gly Pro Gly Leu Leu Ser Arg Leu Gln Gly Phe
 190 195 200

Arg Val Lys Ile Thr Pro Gly Gln Leu Asn Gln Thr Ser Arg Ser
 205 210 215

Pro Val Gln Ile Ser Gly Tyr Leu Asn Arg Thr His Gly Pro Val
 220 225 230

25 Asn Gly Thr His Gly Leu Phe Ala Gly Thr Ser Leu Gln Thr Leu
 235 240 245

Glu Ala Ser Asp Ile Ser Pro Gly Ala Phe Asn Lys Gly Ser Leu
 250 255 260

30 Ala Phe Asn Leu Gln Gly Gly Leu Pro Pro Ser Pro Ser Leu Ala
 265 270 275

35 Pro Asp Gly His Thr Pro Phe Pro Pro Ser Pro Ala Leu Pro Thr
 280 285 290

Thr His Gly Ser Pro Pro Gln Leu His Pro Leu Phe Pro Asp Pro
 295 300 305

40 Ser Thr Thr Met Pro Asn Ser Thr Ala Pro His Pro Val Thr Met
 310 315 320

45 Tyr Pro His Pro Arg Asn Leu Ser Gln Glu Thr
 325 330 335

(2) INFORMATION FOR SEQ ID NO:15:

50 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 241 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Ser Pro Val Ala Pro Ala Cys Asp Pro Arg Leu Leu Asn Lys Leu
1 5 10 15

5 Leu Arg Asp Ser His Leu Leu His Ser Arg Leu Ser Gln Cys Pro
20 25 30

10 Asp Val Asp Pro Leu Ser Ile Pro Val Leu Leu Pro Ala Val Asp
35 40 45

15 Phe Ser Leu Gly Glu Trp Lys Thr Gln Thr Glu Gln Ser Lys Ala
50 55 60

20 Gln Asp Ile Leu Gly Ala Val Ser Leu Leu Leu Glu Gly Val Met
65 70 75

25 Ala Ala Arg Gly Gln Leu Glu Pro Ser Cys Leu Ser Ser Leu Leu
80 85 90

30 Gly Gln Leu Ser Gly Gln Val Arg Leu Leu Leu Gly Ala Leu Gln
95 100 105

35 Gly Leu Leu Gly Thr Gln Leu Pro Leu Gln Gly Arg Thr Thr Ala
110 115 120

40 His Lys Asp Pro Asn Ala Leu Phe Leu Ser Leu Gln Gln Leu Leu
125 130 135

45 Arg Gly Lys Asp Phe Trp Ile Val Gly Asp Glu Leu Gln Cys His
140 145 150

50 Ser Gln Asn Cys Trp Pro Trp Thr Ser Glu Gln Ala Ser Gly Ile
155 160 165

55 Gln Ser Gln Asp Tyr Ser Trp Ser Ala Lys Ser Asn Leu Gln Val
170 175 180

60 Pro Ser Pro Asn Leu Trp Ile Pro Glu Gln Asp Thr Arg Thr Cys
185 190 195

65 Glu Trp Asn Ser Trp Ala Leu Cys Trp Asn Leu Thr Ser Asp Pro
200 205 210

70 Gly Ser Leu Arg His Leu Ala Arg Ser Phe Gln Gln Arg Leu Pro
215 220 225

75 Gly Ile Gln Pro Pro Gly Trp Thr Ser Ser Phe Ser Lys Pro Cys
230 235 240

80 Ser

(2) INFORMATION FOR SEQ ID NO:16:

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 335 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Ser Pro Val Ala Pro Ala Cys Asp Pro Arg Leu Leu Asn Lys Leu
 1 5 10 15

Leu Arg Asp Ser His Leu Leu His Ser Arg Leu Ser Gln Cys Pro
 15 20 25 30

Asp Val Asp Pro Leu Ser Ile Pro Val Leu Leu Pro Ala Val Asp
 20 35 40 45

Phe Ser Leu Gly Glu Trp Lys Thr Gln Thr Glu Gln Ser Lys Ala
 25 50 55 60

Gln Asp Ile Leu Gly Ala Val Ser Leu Leu Glu Gly Val Met
 30 65 70 75

Ala Ala Arg Gly Gln Leu Glu Pro Ser Cys Leu Ser Ser Leu Leu
 35 80 85 90

Gly Gln Leu Ser Gly Gln Val Arg Leu Leu Leu Gly Ala Leu Gln
 40 95 100 105

Gly Leu Leu Gly Thr Gln Leu Pro Leu Gln Gly Arg Thr Thr Ala
 45 110 115 120

His Lys Asp Pro Asn Ala Leu Phe Leu Ser Leu Gln Gln Leu Leu
 50 125 130 135

Arg Gly Lys Val Arg Phe Leu Leu Leu Val Glu Gly Pro Thr Leu
 55 140 145 150

Cys Val Arg Arg Thr Leu Pro Thr Thr Ala Val Pro Ser Ser Thr
 60 155 160 165

Ser Gln Leu Leu Thr Leu Asn Lys Phe Pro Asn Arg Thr Ser Gly
 65 170 175 180

Leu Leu Glu Thr Asn Phe Ser Val Thr Ala Arg Thr Ala Gly Pro
 70 185 190 195

Gly Leu Leu Ser Arg Leu Gln Gly Phe Arg Val Lys Ile Thr Pro

200 205 210
Gly Gln Leu Asn Gln Thr Ser Arg Ser Pro Val Gln Ile Ser Gly
215 220 225
5 Tyr Leu Asn Arg Thr His Gly Pro Val Asn Gly Thr His Gly Leu
230 235 240
10 Phe Ala Gly Thr Ser Leu Gln Thr Leu Glu Ala Ser Asp Ile Ser
245 250 255
Pro Gly Ala Phe Asn Lys Gly Ser Leu Ala Phe Asn Leu Gln Gly
260 265 270
15 Gly Leu Pro Pro Ser Pro Ser Leu Ala Pro Asp Gly His Thr Pro
275 280 285
Phe Pro Pro Ser Pro Ala Leu Pro Thr Thr His Gly Ser Pro Pro
290 295 300
20 Gln Leu His Pro Leu Phe Pro Asp Pro Ser Thr Thr Met Pro Asn
305 310 315
25 Ser Thr Ala Pro His Pro Val Thr Met Tyr Pro His Pro Arg Asn
320 325 330
Leu Ser Gln Glu Thr
335

30 (2) INFORMATION FOR SEQ ID NO:17:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 332 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

40 Ser Pro Ala Pro Pro Ala Cys Asp Pro Arg Leu Leu Asn Lys Leu
1 5 10 15
Leu Arg Asp Ser His Val Leu His Gly Arg Leu Ser Gln Cys Pro
20 25 30
45 Asp Ile Asn Pro Leu Ser Thr Pro Val Leu Leu Pro Ala Val Asp
35 40 45
50 Phe Thr Leu Gly Glu Trp Lys Thr Gln Thr Glu Gln Thr Lys Ala
50 55 60
Gln Asp Val Leu Gly Ala Thr Thr Leu Leu Leu Glu Ala Val Met

65 70 75

5 Thr Ala Arg Gly Gln Val Gly Pro Pro Cys Leu Ser Ser Leu Leu
80 85 90

Val Gln Leu Ser Gly Gln Val Arg Leu Leu Leu Gly Ala Leu Gln
95 100 105

10 Asp Leu Leu Gly Met Gln Leu Pro Pro Gln Gly Arg Thr Thr Ala
110 115 120

15 His Lys Asp Pro Ser Ala Ile Phe Leu Asn Phe Gln Gln Leu Leu
125 130 135

20 Arg Gly Lys Val Arg Phe Leu Leu Leu Val Val Gly Pro Ser Leu
140 145 150

25 Cys Ala Lys Arg Ala Pro Pro Ala Ile Ala Val Pro Ser Ser Thr
155 160 165

Ser Pro Phe His Thr Leu Asn Lys Leu Pro Asn Arg Thr Ser Gly
170 175 180

30 Leu Leu Glu Thr Asn Ser Ser Ile Ser Ala Arg Thr Thr Gly Ser
185 190 195

Gly Phe Leu Lys Arg Leu Gln Ala Phe Arg Ala Lys Ile Pro Gly
200 205 210

35 Leu Leu Asn Gln Thr Ser Arg Ser Leu Asp Gln Ile Pro Gly His
215 220 225

Gln Asn Gly Thr His Gly Pro Leu Ser Gly Ile His Gly Leu Phe
230 235 240

40 Pro Gly Pro Gln Pro Gly Ala Leu Gly Ala Pro Asp Ile Pro Pro
245 250 255

Ala Thr Ser Gly Met Gly Ser Arg Pro Thr Tyr Leu Gln Pro Gly
260 265 270

45 Glu Ser Pro Ser Pro Ala His Pro Ser Pro Gly Arg Tyr Thr Leu
275 280 285

Phe Ser Pro Ser Pro Thr Ser Pro Ser Pro Thr Val Gln Leu Gln
290 295 300

50 Pro Leu Leu Pro Asp Pro Ser Ala Ile Thr Pro Asn Ser Thr Ser
305 310 315

Pro Leu Leu Phe Ala Ala His Pro His Phe Gln Asn Leu Ser Gln

320

325

330

Glu Glu
332

5

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1026 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

15

AGCCCGGCTC CTCCTGCCTG TGACCCCCGA CTCCTAAATA AACTGCTTCG 50

20

TGACTCCCAT GTCCTTCACG GCAGACTGAG CCAGTGCCCA GACATTAACC 100

25

CTTTGTCCAC ACCTGTCCCTG CTGCCTGCTG TGGACTTCAC CTTGGGAGAA 150

30

TGGAAAACCC AGACGGAGCA GACAAAGGCA CAGGATGTCC TGGGAGCCAC 200

AACCCTTCTG CTGGAGGCAG TGATGACAGC ACGGGGACAA GTGGGACCCC 250

35

CTTGCCTCTC ATCCCTGCTG GTGCAGCTT CTGGACAGGT TCGCCTCCTC 300

40

CTCGGGGCC C TGCAGGACCT CCTTGGAAATG CAGCTTCCTC CACAGGAAAG 350

GACCACAGCT CACAAGGATC CCAGTGCCAT CTTCCTGAAC TTCCAACAAC 400

45

TGCTCCGAGG AAAGGTGCGT TTCTGCTCC TTGTAGTGGG GCCCTCCCTC 450

TGTGCCAAGA GGGCCCCACC CGCCATAGCT GTCCCGAGCA GCACCTCTCC 500

50

ATTCCACACA CTGAACAAGC TCCCAAACAG GACCTCTGGA TTGTTGGAGA 550

55

CAAACCTCCAG TATCTCAGCC AGAACTACTG GCTCTGGATT TCTCAAGAGG 600

CTGCAGGCAT TCAGAGCCAA GATTCTGGT CTGCTGAACC AAACCTCCAG 650

5 GTCCCTAGAC CAAATCCCTG GACACCAGAA TGGGACACAC GGACCTTGA 700

GTGGAATTCA TGGACTCTT CCTGGACCCC AACCCGGGGC CCTCGGAGCT 750

10 CCAGACATTC CTCCAGCAAC TTCAGGCATG GGCTCCCGGC CAACCTACCT 800

CCAGCCTGGA GAGTCTCCTT CCCCAGCTCA CCCTTCTCCT GGACGATACA 850

15 CTCTCTTCTC TCCTTCACCC ACCTCGCCCT CCCCCACAGT CCAGCTCCAG 900

20 CCTCTGCTTC CTGACCCCTC TGCGATCACA CCCAACTCTA CCAGTCCTCT 950

TCTATTTGCA GCTCACCCCTC ATTTCCAGAA CCTGTCTCAG GAAGAGTAAG 1000

25 GTGCTCAGAC CCTGCCAACT TCAGCA 1026

30 (2) INFORMATION FOR SEQ ID NO:19:
B |

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1014 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

AGCCCGGCTC CTCCTGCCTG TGACCCCCGA CTCCTAAATA AACTGCTTCG 50

TGACTCCCAT GTCCTTCACG GCAGACTGAG CCAGTGCCCA GACATTAACC 100

45 CTTTGTCCAC ACCTGTCCTG CTGCCTGCTG TGGACTTCAC CTTGGGAGAA 150

TGGAAAACCC AGACGGAGCA GACAAAGGCA CAGGATGTCC TGGGAGCCAC 200

50 AACCCCTTCTG CTGGAGGCAG TGATGACAGC ACGGGGACAA GTGGGACCCC 250

CTTGCCTCTC ATCCCTGCTG GTGCAGCTT CTGGACAGGT TCGCCTCCTC 300
5 CTCGGGGCCC TGCAGGACCT CCTTGGAAATG CAGGGAAGGA CCACAGCTCA 350
CAAGGATCCC AGTGCCATCT TCCTGAACCT CCAACAACTG CTCCGAGGAA 400
10 AGGTGCGTTT CCTGCTCCTT GTAGTGGGGC CCTCCCTCTG TGCCAAGAGG 450
GCCCCACCCG CCATAGCTGT CCCGAGCAGC ACCTCTCCAT TCCACACACT 500
15 GAACAAGCTC CCAAACAGGA CCTCTGGATT GTTGGAGACA AACTCCAGTA 550
TCTCAGCCAG AACTACTGGC TCTGGATTTC TCAAGAGGCT GCAGGCATTC 600
AGAGCCAAGA TTCCTGGTCT GCTGAACCAA ACCTCCAGGT CCCTAGACCA 650
25 AATCCCTGGA CACCAGAATG GGACACACGG ACCCTTGAGT GGAATTCATG 700
GACTCTTCC TGGACCCCAA CCCGGGGCCC TCGGAGCTCC AGACATTCC 750
30 CCAGCAACTT CAGGCATGGG CTCCCGGCCA ACCTACCTCC AGCCTGGAGA 800
1/ Point
35 GTCTCCTTCC CCAGCTCACC CTTCTCCTGG ACGATACACT CTCTCTCTC 850
CTTCACCCAC CTCGCCCTCC CCCACAGTCC AGCTCCAGCC TCTGCTTCCT 900
40 GACCCCTCTG CGATCACACC CAACTCTACC AGTCCTCTTC TATTGCAGC 950
TCACCCCTCAT TTCCAGAACCC TGTCTCAGGA AGAGTAAGGT GCTCAGACCC 1000
45 TGCCAACTTC AGCA 1014
50

(2) INFORMATION FOR SEQ ID NO:20:

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 328 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

15 Ser Pro Ala Pro Pro Ala Cys Asp Pro Arg Leu Leu Asn Lys Leu
 1 5 10 15

20 Leu Arg Asp Ser His Val Leu His Gly Arg Leu Ser Gln Cys Pro
 20 25 30

25 Asp Ile Asn Pro Leu Ser Thr Pro Val Leu Leu Pro Ala Val Asp
 35 40 45

30 Phe Thr Leu Gly Glu Trp Lys Thr Gln Thr Glu Gln Thr Lys Ala
 50 55 60

35 Gln Asp Val Leu Gly Ala Thr Thr Leu Leu Leu Glu Ala Val Met
 65 70 75

40 Thr Ala Arg Gly Gln Val Gly Pro Pro Cys Leu Ser Ser Leu Leu
 80 85 90

45 Val Gln Leu Ser Gly Gln Val Arg Leu Leu Leu Gly Ala Leu Gln
 95 100 105

50 Asp Leu Leu Gly Met Gln Gly Arg Thr Thr Ala His Lys Asp Pro
 110 115 120

55 Ser Ala Ile Phe Leu Asn Phe Gln Gln Leu Leu Arg Gly Lys Val
 125 130 135

60 Arg Phe Leu Leu Leu Val Val Gly Pro Ser Leu Cys Ala Lys Arg
 140 145 150

65 Ala Pro Pro Ala Ile Ala Val Pro Ser Ser Thr Ser Pro Phe His
 155 160 165

70 Thr Leu Asn Lys Leu Pro Asn Arg Thr Ser Gly Leu Leu Glu Thr
 170 175 180

75 Asn Ser Ser Ile Ser Ala Arg Thr Thr Gly Ser Gly Phe Leu Lys
 185 190 195

80 Arg Leu Gln Ala Phe Arg Ala Lys Ile Pro Gly Leu Leu Asn Gln
 200 205 210

85 Thr Ser Arg Ser Leu Asp Gln Ile Pro Gly His Gln Asn Gly Thr
 215 220 225

b |
 cont.

His Gly Pro Leu Ser Gly Ile His Gly Leu Phe Pro Gly Pro Gln
230 235 240

5 Pro Gly Ala Leu Gly Ala Pro Asp Ile Pro Pro Ala Thr Ser Gly
245 250 255

Met Gly Ser Arg Pro Thr Tyr Leu Gln Pro Gly Glu Ser Pro Ser
10 260 265 270

Pro Ala His Pro Ser Pro Gly Arg Tyr Thr Leu Phe Ser Pro Ser
275 280 285

15 Pro Thr Ser Pro Ser Pro Thr Val Gln Leu Gln Pro Leu Leu Pro
290 295 300

Asp Pro Ser Ala Ile Thr Pro Asn Ser Thr Ser Pro Leu Leu Phe
305 310 315

20 Ala Ala His Pro His Phe Gln Asn Leu Ser Gln Glu Glu
320 325 328

(2) INFORMATION FOR SEQ ID NO:21:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

35 Ser Pro Ala Pro Pro Ala Cys Asp Pro Arg Leu Leu Asn Lys Leu
1 5 10 15
Leu Arg Asp Asp His Val Leu His Gly Arg
20 25

(2) INFORMATION FOR SEQ ID NO:22:

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

50 Ser Pro Ala Pro Pro Ala Cys Asp Pro Arg Leu Leu Asn Lys Leu
1 5 10 15
Leu Arg Asp Asp His Ser Val Leu His Gly Arg Leu
20 25 27

(2) INFORMATION FOR SEQ ID NO:23:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Ser Pro Ala Pro Pro Ala Xaa Asp Pro Arg Leu Leu Asn Lys Leu
1 5 10 15
Leu Arg Asp Asp His Val Leu His Gly Arg
20 25

10 (2) INFORMATION FOR SEQ ID NO:24:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Xaa Pro Ala Pro Pro Ala Xaa Asp Pro Arg Leu Xaa Asn Lys
1 5 10 14

25 (2) INFORMATION FOR SEQ ID NO:25:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

1 Pro Arg Leu Leu Asn Lys Leu Leu Arg
5 9

40 (2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 bases
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GCCGTGAAGG ACGTGTCGT CACGAAGCAG TTTATTTAGG AGTCG 45

5 (2) INFORMATION FOR SEQ ID NO:27:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CCNGCNCCNC CNGCNTGYGA 20

15

(2) INFORMATION FOR SEQ ID NO:28:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 bases
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

NCCRTGNARN ACRTGRTCRT C 21

30

(2) INFORMATION FOR SEQ ID NO:29:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 bases
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CCAGCGCCGC CAGCCTGTGA CCCCCGACTC CTAAATAAAC TGCCTCGTGA 50

45

TGACCACGTT CAGCACGGC 69

50

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 bases

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GCCGTGCTGA ACGTGGTCAT CACGAGGCAG TTTATTTAGG AGTCGGGGT 50
10 CACAGGCTGG CGGCGCTGG 69

15 (2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 69 bases
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CCAGCACCTC CGGCATGTGA CCCCCGACTC CTAAATAAAC TGCTTCGTGA 50
30 CGACCACGTC CATCACGGC 69

35 (2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 69 bases
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GCCGTGATGG ACGTGGTCGT CACGAAGCAG TTTATTTAGG AGTCGGGGT 50
45 CACATGCCGG AGGTGCTGG 69

50 (2) INFORMATION FOR SEQ ID NO:33:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 bases
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

10 CCAGCACCGC CGGCATGTGA CCCCCGACTC CTAAATAAAC TGCTTCGTGA 50

CGATCATGTC TATCACGGT 69

15

(2) INFORMATION FOR SEQ ID NO:34:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 bases
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

ACCGTGATAG ACATGATCGT CACGAAGCAG TTTATTTAGG AGTCGGGGGT 50

30

B
1
cont CACATGCCGG CGGTGCTGG 69

35 (2) INFORMATION FOR SEQ ID NO:35:

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 bases
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

45 GCTAGCTCTA GAAATTGCTC CTCGTGGTCA TGCTTCT 37

50 (2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 22 bases
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CAGTCTGCCG TGAAGGACAT GG 22

15 (2) INFORMATION FOR SEQ ID NO:37:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 bases
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

TGTGGACTTT AGCTTGGGAG AATG 24

25 (2) INFORMATION FOR SEQ ID NO:38:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 bases
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

40 GGTCCAGGGA CCTGGAGGTT TG 22

45 (2) INFORMATION FOR SEQ ID NO:39:

50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 bases
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

ATCGATATCG ATAGCCAGAC ACCCCGGCCA G 31

5 (2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 bases
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

15 GCTAGCTCTA GACAGGGAAG GGAGCTGTAC ATGAGA 36

20 (2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: nucleic acid
- 25 (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

30 CTCCTTGGAA CCCAGGGCAG GACC 24
B1
cont.

35 (2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: nucleic acid
- 40 (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

45 GGTCTGCCCT TGGGTTCCAA GGAG 24

50 (2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 27 bases
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

15 CTGCTCCGAG GAAAGGACTT CTGGATT 27

20 (2) INFORMATION FOR SEQ ID NO:44:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 bases
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

35 AATCCAGAAG TCCTTTCCTC GGAGCAG 27

40 (2) INFORMATION FOR SEQ ID NO:45:

45 |
|
B
cont.
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 bases
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

CCCTCTGCGT CGCGGGCGGCC CCACCCAC 28

55 (2) INFORMATION FOR SEQ ID NO:46:

60 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 bases
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GTGGGTGGGG CCGCCGCGAC GCAGAGGG 28

5 (2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 bases
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

15 GACTCGAGGA TCCATCGATT TTTTTTTTTT TTTTT 35

20 (2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 bases
- (B) TYPE: nucleic acid
- 25 (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

30 GACTCGAGGA TCCATCG 17
*B
Pmt*

35 (2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 bases
- (B) TYPE: nucleic acid
- 40 (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

45 GCTAGCTCTA GAAGCCCGGC TCCTCCTGCC TG 32

50 (2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

5
(A) LENGTH: 21 bases
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

CGAAATTAAC CCTCACTAAA G 21

15 (2) INFORMATION FOR SEQ ID NO:51:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

His Val Leu His
1 4

30 25 (2) INFORMATION FOR SEQ ID NO:52:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Ser Arg Leu Ser
1 4

45 (2) INFORMATION FOR SEQ ID NO:53:

50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Ser His Val Leu
1 4

50 (2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

His Ser Arg Leu
1 4

10 (2) INFORMATION FOR SEQ ID NO:55:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Ala Val Asp Phe
1 4

25 (2) INFORMATION FOR SEQ ID NO:56:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Ser Leu Gly Glu
1 4

35 (2) INFORMATION FOR SEQ ID NO:57:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Ala Val Thr Leu
1 4

45 (2) INFORMATION FOR SEQ ID NO:58:

50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Leu Leu Glu Gly
1 4

5 (2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Leu Ser Ser Leu
1 4

15 (2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

25 Leu Gly Gln Leu
1 4

30 (2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Cys Leu Ser Ser
1 4

40 (2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Leu Leu Gly Gln
1 4

50 (2) INFORMATION FOR SEQ ID NO:63:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Ser Ser Leu Leu
1 4

15 (2) INFORMATION FOR SEQ ID NO:64:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Gly Gln Leu Ser
1 4

25 (2) INFORMATION FOR SEQ ID NO:65:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

35 Leu Gln Ser Leu
1 4

35 (2) INFORMATION FOR SEQ ID NO:66:

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Leu Gly Thr Gln
1 4

45 (2) INFORMATION FOR SEQ ID NO:67:

50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Ala Leu Gln Ser
1 4

5

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Leu Leu Gly Thr
1 4

15 (2) INFORMATION FOR SEQ ID NO:69:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Asn Ala Ile Phe
1 4

30 (2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Leu Ser Phe Gln
1 4

40

(2) INFORMATION FOR SEQ ID NO:71:

45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

50 Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys Leu
1 5 10 15

Leu Arg Asp Ser His Val Leu
20 22

5 (2) INFORMATION FOR SEQ ID NO:72:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

His Ser Arg Leu Ser Gln Cys Pro Glu Val His Pro Leu Pro Thr
1 5 10 15
Pro Val Leu Leu Pro Ala Val Asp Phe
20 24

20 (2) INFORMATION FOR SEQ ID NO:73:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Ser Leu Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys Ala Gln
1 5 10 15
Asp Ile Leu Gly Ala Val Thr Leu
20 23

30 (2) INFORMATION FOR SEQ ID NO:74:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln Leu Gly Pro Thr
1 5 10 15
Cys Leu Ser Ser Leu Leu
20 21

45 (2) INFORMATION FOR SEQ ID NO:75:

50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

5 Gly Gln Leu Ser Gly Gln Val Arg Leu Leu Leu Gly Ala Leu Gln
 1 5 10 15

10 Ser
 16

(2) INFORMATION FOR SEQ ID NO:76:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

20 Leu Leu Gly Thr Gln Leu Pro Pro Gln Gly Arg Thr Thr Ala His
 1 5 10 15

25 Lys Asp Pro Asn Ala Ile Phe
 20 22

(2) INFORMATION FOR SEQ ID NO:77:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

35 Leu Ser Phe Gln His Leu Leu Arg Gly Lys Val Arg Phe Leu Met
 1 5 10 15

40 Leu Val Gly Gly Ser Thr Leu Cys Val Arg
 20 25